

11 New osteopontin derived chemotactic and inhibitory peptides useful for
12 promoting scarless wound healing, modulating cellular chemokinesis,
13 promoting formation of atherosclerotic plaques and preventing metastasis
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15 Claim 17: Page 4 v: 6pp: English.
16
17 The present sequence is an osteopontin derived chemotactic peptide.
18 Such chemotactic peptides are useful for promoting scarless wound
19 healing, modulating chemokinesis and promoting cell migration to a wound
20 site in a cell of a subject. They are also used for modulating cellular
21 chemokinesis in a mammalian cell such as smooth muscle cell, a macrophage,
22 an endothelial cell, a vascular cell and a tumorigenic cell. They are
23 useful for treating the formation of atherosclerotic plaques in a
24 subject. The peptides are used for preventing metastasis, treating an
25 atherosclerotic-associated disease such as arthritis, psoriasis, haemorrhoids,
26 tumour metastasis or ocular neovascularisation. They are also used for
27 activating cell apoptosis, for modulating nitrous oxide production and
28 for inducing chemotaxis. The peptides are useful for diagnosing, treating
29 and preventing tumour metastasis, inflammation, osteoporosis and immune
30 diseases. They can also be used to enhance an immune response by
31 attracting macrophages.

32 Sequence 4 AA:

33 Query Match: 100.0%; Score 20; DB 21; Length 4;
34 Best Local Similarity: 100.0%; Pred. No. 6,400,000;
35 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

36 1 VLEP 4

37 1 VLEP 4

38 RESULT 2

39 AAB29558

40 10 AAB29558 standard; peptide; 4 AA.

41 A* AAB29558;

42 14 FEB 2001 (first entry)

43 Adhesion-modulatory peptide; SEQ ID NO:17.

44 Adhesion-modulatory peptide; target cell adhesion to atherosclerotic
45 endothelial cells; fibroblasts; macrophages; neutrophils; monothroblasts;
46 vascular cells; atherosclerotic plaques; atherosclerotic disease;
47 vascular growth; wound healing; keloid formation; scar tissue; fibrosis;
48 anti-inflammation; vascularity; immunomodulatory; anti-inflammatory and vascular
49 immunomodulatory; and CD44 activity; proinflammatory; implant.

50 Synthesized.

51 KW 2000064247 A2.

52 2000064247 A2.

53 17 APR 2001; 2000W6 0510429.

54 16 APR 1999; 9905 0129709.

55 (CHILDREN) CHILDRENS MEDICAL CENT.

56 Ashkar S;

57 WFL: 2001-007002/01.

58 New adhesive modulatory peptides useful for modulating adhesion of
59 target cells such as endothelial cells, fibroblasts, macrophages to
60 substrate such as polyvinyl surfaces, collagen

61 Claim 6: Page 27; 6pp: English.

62 The invention relates to novel adhesion modulatory peptides (AAB29554
63 AAB29558) which modulate the adhesion of a target cell to a substrate.
64 The invention also encompasses substrates and devices treated with a
65 peptide of the inventive compositions comprising a peptide of the
66 invention for in vivo use; and analogues, fragments and chemical
67 derivatives of the peptides of the invention. The peptides are used for
68 modulating the adhesion to a substrate of target cells such as
69 endothelial cells, fibroblasts, macrophages, neutrophils or
70 myofibroblasts. The substrate may be a substrate that is found in the
71 body of a patient, e.g., collagen or hyaluronic acid, or may be a
72 synthetic substrate e.g., a polyvinyl surface, titanium or PSA. The
73 peptides are useful for regulating vessel growth during wound healing
74 and/or in the treatment of damage resulting from vascular disease; for
75 inhibiting or preventing cellular apoptosis; in the treatment of
76 fibrosis, in particular in the clearing of debris; to minimise wound
77 contraction, thereby reducing keloid tissue formation and scarring; and
78 as anti-clotting agents. The peptides also have an immunomodulatory
79 effect, and an anti-fibrotic effect, by adhering to neutrophils.
80 Additionally, peptides of the invention have an anti-tumour effect by
81 competing for alpha v beta 3 integrin binding on the cell surface, and an
82 anti-tumorigenic effect by having anti-CD44 activity. The peptides are
83 useful for stimulating and/or enhancing cell attachment to polymer
84 scaffolds, to enhance tissue growth and for coating medical devices,
85 including prostheses and implants (e.g., vascular implants). The present
86 sequence represents a specifically obtained adhesion modulatory peptide of
87 the invention.

88 Sequence 4 AA:

89 Query Match: 100.0%; Score 20; DB 22; Length 4;

90 Best Local Similarity: 100.0%; Pred. No. 6,400,000;

91 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

92 1 VLEP 4

93 1 VLEP 4

94 RESULT 4

95 AAB29664

96 10 AAB29664 standard; peptide; 4 AA.

97 A* AAB29664;

98 14 FEB 2001 (first entry)

99 Chemotactic peptide pep1.

100 Chemotactic osteopontin; vascularity; anti-arthritis; anti-inflammatory;
101 cytotactic; anti-tumour; anti-inflammatory; osteoporosis;
102 wound healing; cell migration; chemotaxis; atherosclerosis; vascu-

103 KW androgen-associated disease; arthritis; psoriasis; haemorrhoids;
104 KW cellular neovascularisation; cell of fibrosis; atherosclerotic
105 inflammation; osteoporosis; immune disease.

106 Mammalia.

107 Synthesized.

108 KW 2000064247 A2.

109 2000064247 A2.

110 17 APR 2001; 2000W6 0510444.

111 15 APR 1999; 9905 0129764.

112 (CHILDREN) CHILDRENS MEDICAL CENT.

113 Ashkar S;

114 WFL: 2001-007002/01.

115 New osteopontin derived chemotactic and inhibitory peptides; SEQ ID NO: 17.

CC AAbp4-29 standard; Peptide: 9 AA.
 XX
 AC AAbp4-29;
 CC AAbp4-29 (first entry)
 XX
 CC wheat acetyl Coenzyme A carboxylase peptide sequence;
 CC
 XX AAc1; Coenzyme A carboxylase; AcCase; plasmid pK11;
 KW transgenic plant; modified oil content;
 KW polyhydroxyalkanoate polymer; herbicide resistance;
 KW mutant crop improvement;
 XX
 CC Eukaryotic acetyl;
 XX W6529246.A1;
 CC
 CC 02-NOV-1995;
 CC 21-AUG-1994; 94W-03400646;
 CC 21-AUG-1994; 94W-03400646;
 CC (PNE) GENEX LTD;
 CC B114P SWL; Elberton KM; Benton PA; Staban AP;
 CC WPI: 1995 082994/49;
 CC
 CC DNA encoding acetyl Coenzyme A carboxylase used for production
 CC plants with controlled expression of AcCase, esp. for regulation
 CC fatty acid synthesis;
 CC (See, sure; Fig 4; 61pp; English;
 CC
 CC Wheat acetyl Coenzyme A carboxylase (AcCase) was partially
 CC purified from wheat germ and a dominant 220 kDa band was identified
 CC as AcCase by column chromatography and SDS-PAGE. After
 CC purification in the gel, the protein was hydrolysed using
 CC Edman degradation, and resulting peptides were purified by
 CC electrophoresis and loaded onto an ABI 477A pulse liquid
 CC protein sequencer. Sequence data of 4 peptides (this peptide and
 CC peptides AAbp4-29, AAbp4-27 and AAbp4-15) were compared with the
 CC K111 deduced amino acid sequence (AA046101, AAbp4-29, AAbp4-27 and
 CC AAbp4-15) so as to authenticate pK11 (see AAbp4-29 and AAbp4-27
 CC partial cDNA. More specifically, this peptide corresponds to
 CC amino acids 419-427 of the K111 deduced AA sequence. AAbp4-29
 CC (AA046101), partial cDNA clone pK11 (GenBank) and the
 CC used to create a wheat/maize transgenic plant.
 CC transform rate and other oilseed plants (maize, soybean,
 CC sunflower) to downregulate production of the AcCase enzyme.
 CC The transgenic plants have a lower or a modified oil content,
 CC down regulation of oil synthesis can be used to divert the
 CC substrate, acetyl Coenzyme A, into synthesis of alternative
 CC storage materials (starch, protein or novel polymers etc.).
 CC polyhydroxyalkanoates). Full length AcCase clones can be used
 CC to create transgenic plants over-expressing AcCase, and
 CC therefore with increased oil content. AcCase over expression in
 CC wheat plants such as wheat, barley, maize and rice, which are
 CC normally sensitive to herbicides, results in
 CC herbicide resistant plants. AAbp4-29 and AAbp4-15 are normally resistant to these
 CC herbicides).
 XX
 CC Sequence 9 AA;
 CC Query Match 100.0%; Score 20; E-Val 1e-04; Ident 1;
 CC Best Local Similarity 100.0%; Pred. No. 6,4e-05;
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0;
 CC
 CC 1 VLEP 4
 CC 2 VLEP 5

RESULT 7
 AAY07169
 ID AAY07169 standard; Peptide: 13 AA.
 XX
 AC AAY07169;
 CC
 CC 02-JUL-1999 (first entry)
 CC
 CC HLA binding peptide;
 CC
 CC Cancer associated antigen diagnosis, research, treatment, human;
 CC breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
 CC prostate cancer;
 CC
 CC Homo sapiens;
 CC
 CC W6904265.A2;
 CC
 CC 28 JAN 1999;
 CC
 CC 15 JUL 1998; 96W-0514679;
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 CC 22 JUN 1998; 96W-0514679;
 CC 17 JUL 1997; 9708 0896164;
 CC 10 JUL 1997; 9708 0896164;
 CC 10 JUL 1997; 9708 0896164;
 CC 10 JUL 1997; 9708 0896164;
 CC 11 JUL 1997; 9708 0896164;
 CC
 CC (LEW-) LHW13 INS1 VANDER BEEK;
 CC
 CC Chen Y, Gant L, Chen A, O'Hare M, Chata Y, Gold L;
 CC Premschmidt M, Stahl G, Seaman SD, Stockert E;
 CC Turrel O;
 CC WPI: 1999 132439/11;
 CC
 CC New isolated cancer associated nucleic acids and polypeptides;
 CC Isolated using sera from cancer patients, used to develop products
 CC for the diagnosis, monitoring or treatment of cancers
 CC
 CC Example 16, Par 762; 787pp; English;
 CC
 CC The invention relates to a method for diagnosing a disorder characterized
 CC by expression of a human cancer associated antigen precursor, coded for by
 CC a nucleic acid molecule (cDNA), the method comprises: (a) contacting a
 CC biological sample isolated from a subject with an agent that specifically
 CC binds to the NAG, an expression product or a fragment of an expression
 CC product complexed with an HLA molecule; and (b) determining the
 CC interaction between the agent and the NAG of the expression product as a
 CC determination of the disorder, the products and methods can be used in
 CC the diagnosis, monitoring, research, or treatment of conditions
 CC characterized by the expression of various cancer associated antigens.
 CC The invention provides nucleic acid sequences and encoded polypeptides
 CC which are cancer associated antigen precursors expressed in human tissues,
 CC cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
 CC lung cancer.
 CC
 CC Sequence 13 AA;
 CC Query Match 100.0%; Score 23; E-Val 1e-04; Ident 1;
 CC Best Local Similarity 100.0%; Pred. No. 75;
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0;
 CC
 CC 1 VLEP 4
 CC 5 VLEP 8

11 AAY01127 standard; peptide; 10 AA.
 12 AAY 0127;
 13
 14 seq. 2000 (first entry)
 15 HLA binding peptide
 16
 17 amino acid associated with type 1 diabetes; research; treatment; human;
 18 breast cancer; colon cancer; metastatic cancer; renal cancer; lung cancer;
 19 prostate cancer;
 20
 21 B-cell receptors;
 22
 23 W090426; A2;
 24 26 JAN 1999;
 25 15 JUL 1998; 9080 US14679;
 26 22 JUN 1998; 9085 0102422;
 27 17 JUL 1997; 9708 0696164;
 28 10 OCT 1997; 9708 0661599;
 29 10 OCT 1997; 9708 0661765;
 30 10 OCT 1997; 9708 0648705;
 31 11 OCT 1997; 9738 0621697;
 32
 33 (JLOW) EMDIG INS1 CANCER PES;
 34
 35 Chen Y., Gao Y., Puro A., Chaturvedi M., Chaturvedi R.
 36 Proteinase M, 300000, 300000, 300000, 300000, 300000;
 37
 38 W01 1997 152447/1;
 39
 40 New isolated cancer associated nucleic acids and peptides; 14 p;
 41 isolated using sera from cancer patients; used to detect the products
 42 for the diagnosis, monitoring or treatment of cancer;
 43
 44 Example 14; Page 75; 767pp; English;
 45
 46 The invention relates to a method for diagnosing a disorder characterized
 47 by expression of a human cancer associated antigen protein coded for by
 48 a nucleic acid molecule (NAM). The method comprises: (a) contacting a
 49 biological sample isolated from a subject with an agent that specifically
 50 binds to the NAM, an expression product of a treatment of an expression
 51 product complexed with an HLA molecule; and (b) determining the
 52 interaction between the agent and the NAM or the expression product as a
 53 determination of the disorder; the products and methods can be used in
 54 the diagnosis, monitoring, research, or treatment of cancer;
 55 characterized by the expression of various cancer associated antigens;
 56 the invention provides nucleic acid sequences and/or peptides, both
 57 which are cancer associated antigen precursors expressed in human breast
 58 cancer, renal cancer, colon cancer, metastatic cancer, lung cancer, and
 59 other cancer;
 60
 61 Sequence 10 AA;
 62
 63 Query Match 100.0%; Score 20; 10 20; 10 20;
 64 Best Local Similarity 100.0%; Prod. N 10 20;
 65 Matches 4; Conserved 100.0%; Residues 10 20; 10 20;
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 67 1 VLEP 4
 68 1111
 69 5 VLEP 4
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101 of 001 2001 (first entry)
 102
 103 Human transcription factor; treatment; 30; 10; 10;
 104
 105 Human single nucleotide polymorphism (SNP) polymorphic locus;
 106 forensic test; apolipoprotein; 10; 10; 10;
 107
 108 B-cell receptors;
 109
 110 W0200051670 A2;
 111
 112 19 JUL 2001;
 113
 114 05 JAN 2001; 2001W 0800422;
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 116 07 JAN 2000; 2000S-0174 062;
 117
 118 (GURA) CURACEN 0004;
 119
 120 Shinkovsk RA, Leach MD;
 121
 122 W01 2001 451871/48;
 123 N-ES06; AAB09700;
 124
 125 Isolated human polynucleotides containing single nucleotide
 126 polymorphisms, useful for the treatment and diagnosis of viral cancer;
 127 infection and diabetes
 128
 129 Disclosure: Page 42; 47pp; English;
 130
 131 The present invention relates to human nucleic acids containing single
 132 nucleotide polymorphisms (SNPs); these can be used to forecast and
 133 patient tests; and to aid in the treatment of diseases associated with
 134 aberrant protein expression, including cancer, amyloidosis, diabetes,
 135 Alzheimer's disease, hemophilia, osteoarthritis (OA), and arthritis;
 136 stomatocystitis, hemophilia, osteoarthritis, thrombocytopenia, arthritis,
 137 meningitis, muscular disorders, demyelination, neurological diseases, cancer,
 138 osteoporosis, metabolic disorders, hypercholesterolemia, blood pressure disorders,
 139 osteoporosis, pathogenic infections, hypercholesterolemia, obesity, and
 140 autoimmunity. The present sequence is a peptide encoded by a
 141 polymorphism containing of nucleotide treatment of the invention;
 142
 143 Sequence 14 AA;
 144
 145 Query Match 100.0%; Score 20; 10 20; 10 20;
 146 Best Local Similarity 100.0%; Prod. N 10 20;
 147 Matches 4; Conserved 100.0%; Residues 10 20; 10 20;
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 149 1 VLEP 4
 150 1111
 151 5 VLEP 8
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1F 5-DEC-1997; 99AU 000854X.
1R 4-AUG-1999; 99AU 0002014.
XX XX
1A (OYME ) UNIV MEDICORNE.
1A (CSL-) CSL LTD.
1A (GSK) COMMERCIAL SCI & IND RES CORP.
1A (CIB) CHANTIER QUINSLAND INST MEDICAL RES.
1A (BALL ) BALL INST MEDICAL RES WALTER & DEFA.
XX XX
1I Jackson D*, Souravi G, Walker J.
XX XX
XX With Gene 632904/48.
XX XX
1E Nucleo helper cell epitopes derived from canine distemper virus used for
1I preparation of canine vaccines
XX XX
1S Page 1; Page 28; 64pp; English.
XX XX
XX AASv676-helical represent 1 helper cell epitope, derived from canine
XX distemper virus (CDV). Compositions comprising those listed below
XX epitopes are useful for inducing an immune response in animals. The
XX epitopes are useful as components of antibody in particular canine
XX vaccines, either singly or synthetically peptide based vaccines and as
XX additions to vaccines containing more complex antigens.
XX XX
XX Sequence ID: 17 AA.
XX XX
XX Query Match 100.00%; Score 26; 18 21; Length 17.
XX Best Local Similarity 100.00%; Field No. 1; seq2:
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps
XX
1Q 1 VLEP 4
XX 111
1Q 1 VLEP 16
XX
RESULT 11
AASv676.
1E AASv676 standard; pepid: 17 AA.
XX XX
XX AASv676.
XX XX
1E 1-16-2000 (first entry)
XX XX
1E Antigen acid sequence of a helper 1 cell epitope from CDV.
XX XX
XX 1 helper cell epitope; CTV; Immune response; canine vaccines.
XX XX
XX Canine distemper virus.
XX XX
XX W 2; 46390-A1.
XX IN
1E 1-AUG-2000.
XX XX
XX 07-FEB-2000; 2000W; AU00070.
XX XX
XX 05-FEB-1999; 99AU 000854X.
XX EP
XX 04-AUG-1999; 99AU 0002014.
XX PP
XX XX
XX (OYME ) UNIV MEDICORNE.
XX PA
XX (CSL-) CSL LTD.
XX PA
XX (GSK) COMMERCIAL SCI & IND RES CORP.
XX PA
XX (CIB) CHANTIER QUINSLAND INST MEDICAL RES.
XX PA
XX (BALL ) BALL INST MEDICAL RES WALTER & DEFA.
XX XX
XX Jackson D*, Souravi G, Walker J.
XX XX
XX With Gene 632904/48.
XX XX
XX Nucleo helper cell epitopes derived from canine distemper virus used for
XX preparation of canine vaccines .
XX XX
XX Page 1; Page 28; 64pp; English.

```

XX
CV AAW06076 BOR101 represent T helper cell epitopes, derived from varicella
CV distemper virus (VHV). Compositions comprising these T cell helper
CV epitopes are useful for inducing an immune response in an animal. The
CV epitopes are useful as components of animal, in particular, canine
CV vaccines, either simply as synthetic peptide based vaccines and as
CV additions to vaccines containing more complex antigens.

XX
SQ Sequence 17 AA;

Query Match: 100.0%; Score 23.7; E-Val: Length 17;
Best Local Similarity: 100.0%; Pos: 1,36-52;
Matches: 4; Conserved: 0; Mismatches: 0; Indels: 0; Gaps:

CV 1 VIEW 4
111
140 6 VIEW 9

RESULT 12

11 AAW70175 standard; peptides: 19 AA;
AV AAW70175;
XX
XX 07 Dec 1998 (first entry)
XX
XX Internal peptide fragment of GFP 9;
XX
XX Culture filtrate protein: GFP; H37R; 2-1 PAGE; electrophoretic transfer;
XX CV capillary reversed phase chromatography; homology; antigen; antibody;
XX human immunodeficiency virus; HIV.

XX
XX Mycobacterium tuberculosis;
XX
XX W9829132-A1;
XX
XX 09 Jul 1998;
XX
XX 29 Dec 1997; 97W-0524104;
XX
XX 31 Dec 1996; 96S-034503;
XX
XX GENE 3 UNIT NEW YORK STATE;
XX
XX Bellis JJ, Paul S, Zolla-Paerel S;
XX
XX W97: 1999-297797/44;
XX
XX Early detection of mycobacterial infection - by testing a bioherm,
XX fluid sample from a subject for the presence of antibodies reactive
XX with Mycobacterium tuberculosis antigens

XX
XX Example 5; Page 88; 1/0pp; English.

XX
XX Sequences AAW70167-W70179 are internal peptide fragments of selected
XX culture filtrate proteins (CFPs) of M. tuberculosis (MC). Strain H37Rv,
XX determined by LC/MS/MS analysis. To obtain these sequences, the
XX proteins were resolved by 2-D PAGE, transferred to a membrane by
XX electrophoretic transfer, stained, destained, subjected to in-gel proteolytic
XX digestion with trypsin, and then eluted and separated by HPLC using
XX reversed phase chromatography. These antigens and antibodies that form
XX an antigen-antibody complex can be used for the early detection of mycobacterial
XX disease, particularly in subjects infected with human immunodeficiency
XX virus (HIV).

XX
SQ Sequence 19 AA;

Query Match: 100.0%; Score 33.46; E-Val: Length 19;
Best Local Similarity: 100.0%; Pos: 1,50-69;
Matches: 4; Conserved: 0; Mismatches: 0; Indels: 0; Gaps:

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08 protocol: protocol search, using sw model

Path on: October 26, 2002, 00:11:04 : Search time 18 seconds
(without alignment)
7,516 Million seq. of 411/seq

Title: US-09-732-411-15

Perfect score: 20

Sequence: 1 VLEP 4

Scoring table: BLOSUM62

Gapop 10.0 : Gapext 0.5

Scored: 24429 seqs, 2442504 residues

Total number of hits satisfying chosen parameters: 25326

Minimum length: 5

Minimum Match: 40

Maximum Match: 100

First 100 hits: 45, 50, 55, 60, 65, 70, 75, 80, 85, 90

Issued: 10/26/02 14:14:15

Sequence: 1 VLEP 4

Scoring table: BLOSUM62

Gapop 10.0 : Gapext 0.5

Scored: 24429 seqs, 2442504 residues

Total number of hits satisfying chosen parameters: 25326

Minimum length: 5

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Issued: 10/26/02 14:14:15

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Scoring table: BLOSUM62

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Issued: 10/26/02 14:14:15

Sequence: 1 VLEP 4

ALPHABET

RESULT 1

US-09-732-411-15

Sequence: 1 VLEP 4

Scoring table: BLOSUM62

Gapop 10.0 : Gapext 0.5

Scored: 24429 seqs, 2442504 residues

Total number of hits satisfying chosen parameters: 25326

Minimum length: 5

Minimum Match: 40

Maximum Match: 100

First 100 hits: 45, 50, 55, 60, 65, 70, 75, 80, 85, 90

Issued: 10/26/02 14:14:15

Sequence: 1 VLEP 4

Scoring table: BLOSUM62

Gapop 10.0 : Gapext 0.5

Scored: 24429 seqs, 2442504 residues

Total number of hits satisfying chosen parameters: 25326

Minimum length: 5

Minimum Match: 40

Maximum Match: 100

First 100 hits: 45, 50, 55, 60, 65, 70, 75, 80, 85, 90

Issued: 10/26/02 14:14:15

Sequence: 1 VLEP 4

Scoring table: BLOSUM62

Gapop 10.0 : Gapext 0.5

Scored: 24429 seqs, 2442504 residues

Total number of hits satisfying chosen parameters: 25326

Minimum length: 5

Minimum Match: 40

Maximum Match: 100

First 100 hits: 45, 50, 55, 60, 65, 70, 75, 80, 85, 90

Issued: 10/26/02 14:14:15

Sequence: 1 VLEP 4

Scoring table: BLOSUM62

Gapop 10.0 : Gapext 0.5

Scored: 24429 seqs, 2442504 residues

Total number of hits satisfying chosen parameters: 25326

Minimum length: 5

Minimum Match: 40

Maximum Match: 100

First 100 hits: 45, 50, 55, 60, 65, 70, 75, 80, 85, 90

Issued: 10/26/02 14:14:15

Sequence: 1 VLEP 4

Scoring table: BLOSUM62

Gapop 10.0 : Gapext 0.5

Scored: 24429 seqs, 2442504 residues

ALPHABET

RESULT 1

US-09-732-411-15

Sequence: 1 VLEP 4

Scoring table: BLOSUM62

Gapop 10.0 : Gapext 0.5

Scored: 24429 seqs, 2442504 residues

Total number of hits satisfying chosen parameters: 25326

Minimum length: 5

Minimum Match: 40

Maximum Match: 100

First 100 hits: 45, 50, 55, 60, 65, 70, 75, 80, 85, 90

Issued: 10/26/02 14:14:15

Sequence: 1 VLEP 4

Scoring table: BLOSUM62

Gapop 10.0 : Gapext 0.5

Scored: 24429 seqs, 2442504 residues

Total number of hits satisfying chosen parameters: 25326

Minimum length: 5

Minimum Match: 40

Maximum Match: 100

First 100 hits: 45, 50, 55, 60, 65, 70, 75, 80, 85, 90

Issued: 10/26/02 14:14:15

Sequence: 1 VLEP 4

Scoring table: BLOSUM62

Gapop 10.0 : Gapext 0.5

Scored: 24429 seqs, 2442504 residues

Total number of hits satisfying chosen parameters: 25326

Minimum length: 5

Minimum Match: 40

Maximum Match: 100

First 100 hits: 45, 50, 55, 60, 65, 70, 75, 80, 85, 90

Issued: 10/26/02 14:14:15

Sequence: 1 VLEP 4

Scoring table: BLOSUM62

Gapop 10.0 : Gapext 0.5

Scored: 24429 seqs, 2442504 residues

Total number of hits satisfying chosen parameters: 25326

Minimum length: 5

Minimum Match: 40

Maximum Match: 100

First 100 hits: 45, 50, 55, 60, 65, 70, 75, 80, 85, 90

Issued: 10/26/02 14:14:15

Sequence: 1 VLEP 4

Scoring table: BLOSUM62

Gapop 10.0 : Gapext 0.5

Scored: 24429 seqs, 2442504 residues

```

11      1 VLEP 4
12      1 MOLECULE TYPE: peptide
13      US-09-732-411-15-009 20

Query Match
Best Local Similarity 100.00; Score 20; DB 1; Length 25;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

14      1 VLEP 4
15      1 III
16      4 VLEP 7

RESULT 4
17      17 17 17 17 20
18      1 Sequence 20; Application US/09457363
19      1 Patent No. 6824647
20      1 GENERAL INFORMATION:
21      1 APPLICANT: Postlethwaite, Arnold E.
22      1 APPLICANT: Seyer, Jerome
23      1 APPLICANT: Kadz, Andrew
24      1 TITLE OF INVENTION: CHEMOTACTIC WOUND HEALING PEPTIDES
25      1 NUMBER OF SEQUENCES: 25
26      1 CORRESPONDENCE ADDRESS:
27      1 ADDRESSEE: Scully, Scott, Murphy & Presser
28      1 STREET: 400 Garden City Plaza
29      1 CITY: Garden City
30      1 STATE: New York
31      1 COUNTRY: U.S.A.
32      1 ZIP: 11540
33      1 COMPUTER READABLE FORM:
34      1 MEDIUM TYPE: Floppy disk
35      1 COMPUTER: IBM PC compatible
36      1 OPERATING SYSTEM: PC DOS/MS DOS
37      1 SOFTWARE: Patent Release #1.0, Version #1.25
38      1 CURRENT APPLICATION DATA:
39      1 APPLICATION NUMBER: 09/09457363
40      1 FILING DATE:
41      1 CLASSIFICATION: 530
42      1 CLASSIFICATION INFORMATION:
43      1 NAME: DiGilio, Frank S.
44      1 REGISTRATION NUMBER: 41,846
45      1 REFERENCE/SEQUENCE NUMBER: 90202
46      1 TELEPHONE: (516) 742-4343
47      1 TELEFAX: (516) 742-4344
48      1 TELETYPE: 240 961 SANS DR
49      1 INFORMATION FOR SEQ ID NO: 20:
50      1 SEQUENCE CHARACTERISTICS:
51      1 LENGTH: 25 amino acids
52      1 TYPE: amino acid
53      1 TOPOLOGY: linear
54      1 MOLECULE TYPE: peptide
55      1 US 09 457 363 20

Query Match
Best Local Similarity 100.00; Score 20; DB 2; Length 25;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

16      1 VLEP 4
17      1 III
18      4 VLEP 7

RESULT 5
19      17 17 17 17 25
20      1 Sequence 5; Application US/0911626
21      1 Patent No. 600172
22      1 GENERAL INFORMATION:
23      1 APPLICANT: BOTH, GERALD W.
24      1 TITLE OF INVENTION: GENE THERAPY USING AVIAN ALTERNATE VECTORS
25      1 FILE REFERENCE: Gene Therapy Using Avian Altrnate Vc
26      1 CURRENT APPLICATION NUMBER: 09/0911626
27      1 CURRENT FILING DATE: 1998 04 20

```



```

1  SOFTWARE: Patent In Release #1.0, Version #1.25
2  CURRENT APPLICATION DATA:
3  APPLICATION NUMBER: US/09/767,508
4  FILING DATE:
5  CLASSIFICATION: 435
6  PRIOR APPLICATION DATA:
7  APPLICATION NUMBER: 09/62,833
8  FILING DATE: 13 No. 591057/number 1995
9  ALL RELY/AGENT INFORMATION:
10 NAME: Darby, J. James D.
11 REGISTRATION NUMBER: 43,674
12 REFERENCE/AGENT NUMBER: 4755, P. 02
13 TELECOMMUNICATION INFORMATION:
14 TELEPHONE: 616-843-2210
15 TELEFAX: 616-843-8897
16
17 INFORMATION FOR SEQ ID NO: 1:
18 SEQUENCE CHARACTERISTICS:
19 LENGTH: 41 amino acids
20 TYPE: amino acid
21 STRANDEDNESS: linear
22 TOPOLOGY: linear
23 MOLECULE TYPE: peptide
24
25

```

```

Query Match: 100.0%, Score 20; DR 2; Length 41
Best Local Similarity: 100.0%; Prod. No. 1,1e-02;
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0

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07 1 VLEP 4
08 1 111
09 7 VLEP 10

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10 1 111
11 7 VLEP 10

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RESULT 10

```

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US/09/767,508-1

```

```

1 Sequence 1: Application US/09/767,508
2 Patent No. 628782
3 GENERAL INFORMATION:
4 APPLICANT: The Upjohn Company
5 TITLE OF INVENTION: A Cloned DNA Encoding a VPP GARNET
6 NUMBER OF INVENTORS: 19
7 ADDRESS: The Upjohn Company, Intellectual
8 ADDRESS: Property Law
9 STREET: 401 Henrietta Street
10 CITY: Kalamazoo
11 STATE: Michigan
12 COUNTRY: USA
13 ZIP: 49001
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: floppy disk
16 OPERATING SYSTEM: IBM PC/XT/AT
17 SOFTWARE: Patent In Release #1.0, Version #1.25
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/09/767,508
20 FILING DATE:
21 CLASSIFICATION:
22 ALL RELY/AGENT INFORMATION:
23 NAME: Darby, J. James D.
24 REGISTRATION NUMBER: 43,674
25 REFERENCE/AGENT NUMBER: 4755, P. 02
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE: 616-843-2210
28 TELEFAX: 616-843-8897
29
30 INFORMATION FOR SEQ ID NO: 1:

```

```

1  SEQUENCE CHARACTERISTICS:
2  LENGTH: 41 amino acids
3  TYPE: amino acid
4  STRANDEDNESS: linear
5  TOPOLOGY: linear
6  MOLECULE TYPE: peptide
7  US/09/767,508-1

```

```

Query Match: 100.0%, Score 20; DR 2; Length 41
Best Local Similarity: 100.0%; Prod. No. 1,1e-02;
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0

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07 1 VLEP 4
08 1 111
09 7 VLEP 10

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10 1 111
11 7 VLEP 10

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RESULT 10

```

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US/09/767,508-1

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1 Sequence 1: Application US/09/767,508
2 Patent No. 628782
3 GENERAL INFORMATION:
4 APPLICANT: The Upjohn Company
5 TITLE OF INVENTION: A Cloned DNA Encoding a VPP GARNET
6 NUMBER OF INVENTORS: 19
7 ADDRESS: The Upjohn Company, Intellectual
8 ADDRESS: Property Law
9 STREET: 401 Henrietta Street
10 CITY: Kalamazoo
11 STATE: Michigan
12 COUNTRY: USA
13 ZIP: 49001
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: floppy disk
16 OPERATING SYSTEM: IBM PC/XT/AT
17 SOFTWARE: Patent In Release #1.0, Version #1.25
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/09/767,508
20 FILING DATE:
21 CLASSIFICATION:
22 ALL RELY/AGENT INFORMATION:
23 NAME: Darby, J. James D.
24 REGISTRATION NUMBER: 43,674
25 REFERENCE/AGENT NUMBER: 4755, P. 02
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE: 616-843-2210
28 TELEFAX: 616-843-8897
29
30 INFORMATION FOR SEQ ID NO: 1:

```

```

Query Match: 100.0%, Score 20; DR 2; Length 41
Best Local Similarity: 100.0%; Prod. No. 1,1e-02;
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0

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07 1 VLEP 4
08 1 111
09 7 VLEP 10

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10 1 111
11 7 VLEP 10

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RESULT 11

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US/09/767,508-1

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1 Sequence 1: Application US/09/767,508
2 Patent No. 628782

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1 GENERAL INF:PMAL:NE
2 APPLICANT: Bartholomew, Sharon
3 APPLICANT: Bartholomew, Kelly
4 APPLICANT: Bartholomew, Kelly
5 APPLICANT: Bartholomew, Kelly
6 APPLICANT: Bartholomew, Kelly
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98 APPLICANT: Bartholomew, Kelly
99 APPLICANT: Bartholomew, Kelly
100 APPLICANT: Bartholomew, Kelly

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Query Match: 100.0% Score: 200 Length: 400
Best Local Similarity: 100.0% Prod. No. 1200021
Matches: 4 Conserved: 0 Mismatches: 0 Gaps: 0

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1 VLEP 4

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1 VLEP 4

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1 VLEP 4

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Query Match: 100.0% Score: 200 Length: 400
Best Local Similarity: 100.0% Prod. No. 1200021
Matches: 4 Conserved: 0 Mismatches: 0 Gaps: 0

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1 VLEP 4

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1 AGENCY/ALIAN NUMBER: BR 40/026,100
 2 FILING DATE: 15 SEP 1996
 3 AGENCY/ALIAN INFORMATION:
 4 NAME: Mandragoras, Amy E.
 5 REGISTRATION NUMBER: 46,207
 6 REFERENCE NUMBER: LEN-020
 7 TELECOMMUNICATION INFORMATION:
 8 TELEPHONE: (617)227-7400
 9 TELEFAX: (617)42-4214
 10 INFORMATION FOR SEQ ID NO: 1:
 11 SEQUENCE CHARACTERISTICS:
 12 LENGTH: 75 amino acids
 13 TYPE: amino acid
 14 CYCLE: Linear
 15 MODIFIABLE TYPE: peptide
 16 FRAGMENT TYPE: internal
 17 US 09-732-411-15

Query Match: 100.00; Score 20; DB 4; Length 75;
 Best Local Similarity: 100.00; Pred. No. 2,600,02;
 Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

17 1 VLEP 4
 18 111
 19 25 VLEP 25

Search completed: October 28, 2002, 06:17:41
 24 files, 16 secs

Genature version 5.1.3
Copyright (c) 1999-2002 Genature, Inc.

Maximum protein-protein search, using 82 model

Run on: October 28, 2002, 06:24:25 : Search time 47 seconds
(without annotations)
8.178 Million cell 4.444e5/seq

Title: US 09 732-411-15

Protein source: 20

Sequence: 1 VLEP 4

Scoring table: BLOSUM62
Gapop (6,0) : Gapext 0.5

Searches: 241 for seqs, 960944 residues

Total number of hits satisfying chosen parameters: 00

Minimum identity length: 1
Minimum E value: 1

Post processing: Minimum Match 04
Maximum Match 1000
Listing first 45 summaries

Database: 1 PIR/UniProt
1: PIR/UniProt
2: PIR/UniProt
3: PIR/UniProt
4: PIR/UniProt

Prod. No. is the number of results predicted by database search.
Score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	12	60.0	3	3	A3802	thyrotropin-releasing hormone-like peptide, rabbit
2	11	55.0	4	2	U1049	thyrotropin-releasing hormone-like peptide, rabbit
3	11	60.0	4	2	U1049	thyrotropin-releasing hormone-like peptide, rabbit
4	9	40.0	4	2	A02147	thyrotropin-releasing hormone-like peptide, rabbit
5	9	55.0	3	3	PIR/UniProt	thyrotropin-releasing hormone-like peptide, rabbit
6	9	55.0	3	3	PIR/UniProt	thyrotropin-releasing hormone-like peptide, rabbit
7	9	55.0	3	3	PIR/UniProt	thyrotropin-releasing hormone-like peptide, rabbit
8	9	55.0	3	3	PIR/UniProt	thyrotropin-releasing hormone-like peptide, rabbit
9	9	55.0	3	3	PIR/UniProt	thyrotropin-releasing hormone-like peptide, rabbit
10	9	55.0	3	3	PIR/UniProt	thyrotropin-releasing hormone-like peptide, rabbit
11	9	55.0	3	3	PIR/UniProt	thyrotropin-releasing hormone-like peptide, rabbit
12	9	55.0	3	3	PIR/UniProt	thyrotropin-releasing hormone-like peptide, rabbit
13	9	55.0	3	3	PIR/UniProt	thyrotropin-releasing hormone-like peptide, rabbit
14	9	55.0	3	3	PIR/UniProt	thyrotropin-releasing hormone-like peptide, rabbit
15	9	55.0	3	3	PIR/UniProt	thyrotropin-releasing hormone-like peptide, rabbit
16	9	55.0	3	3	PIR/UniProt	thyrotropin-releasing hormone-like peptide, rabbit
17	9	55.0	3	3	PIR/UniProt	thyrotropin-releasing hormone-like peptide, rabbit
18	9	55.0	3	3	PIR/UniProt	thyrotropin-releasing hormone-like peptide, rabbit
19	9	55.0	3	3	PIR/UniProt	thyrotropin-releasing hormone-like peptide, rabbit
20	9	55.0	3	3	PIR/UniProt	thyrotropin-releasing hormone-like peptide, rabbit
21	9	55.0	3	3	PIR/UniProt	thyrotropin-releasing hormone-like peptide, rabbit
22	9	55.0	3	3	PIR/UniProt	thyrotropin-releasing hormone-like peptide, rabbit
23	9	55.0	3	3	PIR/UniProt	thyrotropin-releasing hormone-like peptide, rabbit
24	9	55.0	3	3	PIR/UniProt	thyrotropin-releasing hormone-like peptide, rabbit
25	9	55.0	3	3	PIR/UniProt	thyrotropin-releasing hormone-like peptide, rabbit
26	9	55.0	3	3	PIR/UniProt	thyrotropin-releasing hormone-like peptide, rabbit
27	9	55.0	3	3	PIR/UniProt	thyrotropin-releasing hormone-like peptide, rabbit
28	9	55.0	3	3	PIR/UniProt	thyrotropin-releasing hormone-like peptide, rabbit
29	9	55.0	3	3	PIR/UniProt	thyrotropin-releasing hormone-like peptide, rabbit

RESULT 1

A3802

thyrotropin-releasing hormone-like peptide, rabbit

Species: thyrotropin-releasing hormone-like peptide, rabbit

Created: 15 Jun 2002; sequence revision: 15 Jun 2002; entry status: experimental

Accession: A3802

Accession: A3802

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Accession: A3802

C:Accession: A61300
 C:Field: R.; Ethna, Y.; Niki, T.; Nakamura, T.; Nakamura, A.
 J. Biochem. 92, 1059-1068, 1982
 A:Title: Purification and characterization of a protein from *Escherichia coli* which forms a complex with DNA
 A:Reference number: A61300; MUID:83082696
 A:Accession: A61300
 A:Molecule type: protein
 A:Residues: 1-4 <KIS>
 C:Comment: This protein resembles some of the histone like protein of bacteria in amino acid sequence
 C:Keywords: DNA binding; monomer

Query Match 35.0%; Score 7; DB 2; Length 4;
 Best local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Q7 2 LE 3
 1
 1 ME 2

RESULT 14

157745
 D-mannanase hydrolase (xuaA) *Escherichia coli*
 C:Species: *Escherichia coli*
 C:Date: 07-Jun-1996 #sequence_revision 07 Jun 1996 #text_change 08 Oct 1999
 C:Accession: 157745
 R:Blanco, C.; Ritzenthaler, P.; Kolb, A.
 Mol. Gen. Genet. 202, 112-119, 1986
 A:Title: The regulatory region of the xuaA operon in *Escherichia coli* K12.
 A:Reference number: 157745; MUID:86174344
 A:Accession: 157745
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-4 <RES>
 A:Notes references: DMLX:AC3411, NID:445300, ELDN:GA27147.1; FID:Q581254

Query Match 35.0%; Score 7; DB 2; Length 4;
 Best local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Q7 2 LE 3
 1
 1 ME 2

RESULT 15

533508
 Starvation-induced ribonuclease - tomato
 C:Species: *Lycopersicon esculentum* (tomato)
 C:Date: 07 Aug 1995 #sequence_revision 07 Sep 1995 #text_change 07 May 1999
 C:Accession: S53508
 R:Koeck, M.; Loeffler, A.; Abel, S.; Glund, K.
 Plant Mol. Biol. 27, 477-485, 1995
 A:Title: cDNA structure and regulatory properties of a family of starvation induced ribonucleases
 A:Reference number: S53506; MUID:95201242
 A:Accession: S53508
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-4 <KOE>

Query Match 35.0%; Score 7; DB 2; Length 4;
 Best local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q7 4 P 4
 1
 2 P 2

Search completed: October 28, 2002, 06:27:18
 Job time : 50 secs

DE Carbon monoxide dehydrogenase small chain (P11299) (Fragment).
 OS Escherichia coli O157:H7.
 OC Bacterium: Proteobacteria.
 CX NCBI TaxId 2002.
 RN 111
 RP SEQUENCE.
 EX MEDLINE 9206676; PubMed 9206676.
 RA Krieger M., Borker S., Meyer G.,
 RI "Biochemistry and distribution of carbonic dehydratase structural genes in
 PI Escherichia coli O157:H7." *Arch. Microbiol.* 152:335-341(1999).
 RL 1. "CARBONIC DEHYDRATASE (CDH) IN ESCHERICHIA COLI O157:H7."
 OS Escherichia coli O157:H7.
 OC Bacterium: Proteobacteria.
 CX NCBI TaxId 2002.
 RN 111
 RP SEQUENCE.
 EX MEDLINE 9206676; PubMed 9206676.
 RA Krieger M., Borker S., Meyer G.,
 RI "Biochemistry and distribution of carbonic dehydratase structural genes in
 PI Escherichia coli O157:H7." *Arch. Microbiol.* 152:335-341(1999).
 RL 1. "CARBONIC DEHYDRATASE (CDH) IN ESCHERICHIA COLI O157:H7."
 OS Escherichia coli O157:H7.
 OC Bacterium: Proteobacteria.
 CX NCBI TaxId 2002.
 RN 111
 RP SEQUENCE.
 EX MEDLINE 9206676; PubMed 9206676.
 RA Krieger M., Borker S., Meyer G.,
 RI "Biochemistry and distribution of carbonic dehydratase structural genes in
 PI Escherichia coli O157:H7." *Arch. Microbiol.* 152:335-341(1999).
 RL 1. "CARBONIC DEHYDRATASE (CDH) IN ESCHERICHIA COLI O157:H7."

Query Match: 100% Score 21 DB 11 Length 41
 Best Local Similarity: 100% Pred. No. 100%
 Matches 0; Conservation 1; Mismatches 0; Gaps 0

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RESULT 1:
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 DE 01 NOV 1995 (Ref. 42, Created)
 RI 01 NOV 1995 (Ref. 42, Last sequence update)
 PI 01 NOV 1995 (Ref. 42, Last annotation update)
 DE EMPLOYEE like neuropeptide YMRP amide.
 OS Hirudo medicinalis (Medicinal leech).
 OC Arthropoda: Malacostraca: Hirudinoidea: Hirudinea.
 CX NCBI TaxId 6421.
 RN 111
 RP SEQUENCE.
 EX MEDLINE 9206676; PubMed 1666945.
 RA Evans B., Borker S., Meyer G.,
 RI "Biochemistry and distribution of carbonic dehydratase structural genes in
 PI Escherichia coli O157:H7." *Arch. Microbiol.* 152:335-341(1999).
 RL 1. "CARBONIC DEHYDRATASE (CDH) IN ESCHERICHIA COLI O157:H7."

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 Matches 0; Conservation 1; Mismatches 0; Gaps 0

QY 2 1 2
 DB 2 M 2

RESULT 1:
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 A: 100482
 DE 01 NOV 1995 (Ref. 42, Created)
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 DE EMPLOYEE like neuropeptide YMRP amide.
 OS Hirudo medicinalis (Medicinal leech).
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 EX MEDLINE 9206676; PubMed 1666945.
 RA Evans B., Borker S., Meyer G.,
 RI "Biochemistry and distribution of carbonic dehydratase structural genes in
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 RL 1. "CARBONIC DEHYDRATASE (CDH) IN ESCHERICHIA COLI O157:H7."

OS Hirudo medicinalis (Medicinal leech).
 OC Escherichia coli O157:H7.
 OC Bacterium: Proteobacteria.
 CX NCBI TaxId 2002.
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 RP SEQUENCE.
 EX MEDLINE 9206676; PubMed 9206676.
 RA Krieger M., Borker S., Meyer G.,
 RI "Biochemistry and distribution of carbonic dehydratase structural genes in
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Query Match: 100% Score 21 DB 11 Length 41
 Best Local Similarity: 100% Pred. No. 100%
 Matches 0; Conservation 1; Mismatches 0; Gaps 0

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RESULT 1:
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 PI 01 NOV 1995 (Ref. 42, Last annotation update)
 DE EMPLOYEE like neuropeptide YMRP amide.
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 OC Arthropoda: Malacostraca: Hirudinoidea: Hirudinea.
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 EX MEDLINE 9206676; PubMed 1666945.
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RESULT 1:
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 RA Evans B., Borker S., Meyer G.,
 RI "Biochemistry and distribution of carbonic dehydratase structural genes in
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 RL 1. "CARBONIC DEHYDRATASE (CDH) IN ESCHERICHIA COLI O157:H7."

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>X NCB_LexID 89766;
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>EN SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION: N.
>EN LIVER Brain;
>EX EMBL 107604;
>FA Iwaki Shi E., Hisada M., Minakata H.;
>EN "Cardiac peptides isolated from the brain of a dog nose leishmaniasis,
>EN peptides minor,"
>EN Peptides 21:624-630(2000).
>EN 1- FUNCTION: Cardioactive; has both positive chronotropic and
>EN inotropic effects on the heart. Ocp-2 is a 1000 time less
>EN active than Ocp-1.
>EN 2- SUBCELLULAR LOCATION: Secreted.
>EN 3- PTM: Ocp-2 has L-Phe instead of D-Phe.
>EN 4- MASS SPECTROMETRY: MW 395.2; MTRKD NALLD.
>KW Hormone; D-amino acid.
>PI M_2383 2 2 1; PHENYLALANINE.
>Y SEQUENCE 4 AA: 394 MW: 6667908100000000 (Ocp-4)

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>Query Match 10.0% Score 2; DB 1; Length 4;
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>L 4 F 4

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>Search completed: October 28, 2002, 06:25:54
>Run time : 14 secs

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11 New, state-of-the-art, chemotactic and inhibitory peptides, useful for
12 treatment of metastatic disease, modulating cellular growth and
13 preventing formation of atherosclerotic plaques and preventing metastasis
14
15 (Claim 1); Page 43; 6pp; English.
16
17 The present sequence is an osteopontin-derived chemotactic peptide,
18 used, chemotactic peptides are useful for promoting starless wound
19 healing, modulating chemotaxis and promoting cell attachment to a
20 surface of a cell of a subject, they are also used for promoting cell
21 attachment to a mammalian cell, such as smooth muscle cells, a macrophage,
22 an endothelial cell, a vascular cell, and a tumor necrosis cell, they are
23 used for treating the formation of atherosclerotic plaques in a
24 subject. The peptides are used for preventing metastasis, preventing
25 metastatic disease, such as epithelial, mesothelial, hematolymphoid,
26 tumor metastasis or ocular neovascularization, they are also used for
27 preventing cell apoptosis, for modulating nitric oxide production and
28 for inducing chemotaxis. The peptides are useful for diagnosing, treating
29 and preventing tumor metastasis, inflammation, angiogenesis and tumor
30 diseases, they can also be used to enhance an immune response by
31 attracting macrophages.
32 Sequence: 4 AA;
33
34 Query Match: 100.0%; Score 20; DB 21; Length 4;
35 Best Local Similarity: 100.0%; Pred. No. 6.4e+05;
36 Matches: 4; Conservative 0; Mismatches 0; Indels 1; Gaps 0;
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38 QY 1 VLEP 4
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40 1 VLEP 4
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100 14-SEP-2001 (first entry)

101 the invention relates to novel, adhesion, modulatory peptides (AAB25558-
102 AAB25558) which mediate the adhesion of a target cell to a substrate.
103 The invention also encompasses substrates and devices treated with a
104 peptide of the invention compositions comprising a peptide of the
105 invention for in vivo use; and analogues, fragments and chemical
106 derivatives of the peptides of the invention. The peptides are used for
107 modulating the adhesion to a substrate of target cells such as
108 endothelial cells, fibroblasts, macrophages, neutrophils or
109 myofibroblasts. The substrate may be a substrate that is found in the
110 body of a patient, e.g., collagen or hyaluronate, or may be a
111 synthetic substrate, e.g., a polymeric surface, e.g., a film. The
112 peptides are useful for repairing vessel growth during wound healing
113 and/or in the treatment of damage resulting from vascular diseases, e.g.,
114 inhibiting or preventing cellular apoptosis in the treatment of
115 fibrosis. In particular, in the treatment of diabetes, diabetes-related
116 contraction, thereby reducing keloid tissue formation and scar tissue
117 and in clotting agents, the peptides also have an immunomodulatory
118 effect, and an antifibrotic effect by adhering to neutrophils.
119 Additionally, peptides of the invention have an antitumor effect by
120 competing for alpha-vitronectin binding in the cell surface, and an
121 antitumor effect by having anti-CD44 activity. The peptides are
122 useful for stimulating and/or enhancing cell attachment to polymer
123 scaffolds, to enhance tissue growth and for coating medical devices,
124 including prostheses and implants (e.g., vascular implants). The present
125 sequence represents a specifically obtained adhesion modulatory peptide
126 the invention.
127 Sequence: 4 AA;
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130 Best Local Similarity: 100.0%; Pred. No. 6.4e+05;
131 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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[illegible][illegible]

XX
IN WOLFGANG, A.
XX
... 6336 1000

[illegible]
$$\begin{aligned} \mathbb{E}[\mathbf{Y}_1] &= \mathbb{E}[\mathbf{Y}_2] = \mathbf{0}, \quad \mathbb{E}[\mathbf{Y}_1 \mathbf{Y}_1^T] = \mathbf{I}_2, \quad \mathbb{E}[\mathbf{Y}_1 \mathbf{Y}_2^T] = \mathbf{0}, \\ \mathbb{E}[\mathbf{Y}_1 \mathbf{Y}_2^T] &= \mathbf{0}, \quad \mathbb{E}[\mathbf{Y}_1 \mathbf{Y}_1^T] = \mathbf{I}_2, \quad \mathbb{E}[\mathbf{Y}_2 \mathbf{Y}_2^T] = \mathbf{I}_2, \end{aligned}$$
[illegible]

New fluorometric or fluorosensory reported molecules:
claim 6; Page 163; 00444; English.

AAV15618.Y15799 represents polypeptides used to make a fluorescent reporter molecules of the invention, which molecules contain a peptide moiety (e.g., present sequence) which acts as a substrate for enzymes involved in synthesis of a peptide or polypeptide. The compounds can be used as a reagent of fluorescent substrates for enzymes, depending on the peptide moiety used, the fluorescent molecules can be used for detection of measuring the activity of an enzyme involved in the synthesis as well as to determine whether a test compound has an effect on an enzyme involved in the synthesis cascade in cells; for determining the sensitivity of an animal with respect to treatment with chemical treatment or determining whether a test substance exhibits a toxicity, causes a enhances cell death, or test cells; for detection of measuring the activity of a viral protease in cells; for determining whether a test compound has an effect on the activity of a viral protease in cells; and for measuring the activity of a determined whether a test substance has an effect on the activity of a protease or peptidase in cells.

[illegible]

Query Match	70.0%	Score: 14	100%	Length: 4
Best Local Similarity	66.7% <td>Score: 10 <td>100% <th>Length: 4</th> </td></td>	Score: 10 <td>100% <th>Length: 4</th> </td>	100% <th>Length: 4</th>	Length: 4
Matches	27	Outliers: 1	Mismatches: 0	High: 15

☐ Yes

[illegible] $\lambda_{\text{max}} = 280 \text{ nm}$

$\mathcal{C} = \{C_1, \dots, C_n\}$

XX
XX

[illegible][illegible]

1. *Phragmites australis* (Cav.) Trin. ex Steud.

[illegible][illegible]

WILLIAMS, L. A. 7 A2.

$$| \rangle = A | E_{\text{max}} \rangle + B | E_{\text{min}} \rangle + C | S_0 \rangle + D | S_1 \rangle,$$

Figure 1. The effect of the concentration of the *Ag* on the *Ag* concentration of the *Ag* solution.

WALSH (1971) CHILDE'S BOOKS, 1971.

$$A_i \cap K_i = \emptyset$$
$$N = N_1 \cup N_2 \cup N_3 \cup N_4 \cup N_5 \cup N_6 \cup N_7 \cup N_8 \cup N_9 \cup N_{10} \cup N_{11} \cup N_{12} \cup N_{13} \cup N_{14} \cup N_{15} \cup N_{16} \cup N_{17} \cup N_{18} \cup N_{19} \cup N_{20} \cup N_{21} \cup N_{22} \cup N_{23} \cup N_{24} \cup N_{25} \cup N_{26} \cup N_{27} \cup N_{28} \cup N_{29} \cup N_{30} \cup N_{31} \cup N_{32} \cup N_{33} \cup N_{34} \cup N_{35} \cup N_{36} \cup N_{37} \cup N_{38} \cup N_{39} \cup N_{40} \cup N_{41} \cup N_{42} \cup N_{43} \cup N_{44} \cup N_{45} \cup N_{46} \cup N_{47} \cup N_{48} \cup N_{49} \cup N_{50} \cup N_{51} \cup N_{52} \cup N_{53} \cup N_{54} \cup N_{55} \cup N_{56} \cup N_{57} \cup N_{58} \cup N_{59} \cup N_{60} \cup N_{61} \cup N_{62} \cup N_{63} \cup N_{64} \cup N_{65} \cup N_{66} \cup N_{67} \cup N_{68} \cup N_{69} \cup N_{70} \cup N_{71} \cup N_{72} \cup N_{73} \cup N_{74} \cup N_{75} \cup N_{76} \cup N_{77} \cup N_{78} \cup N_{79} \cup N_{80} \cup N_{81} \cup N_{82} \cup N_{83} \cup N_{84} \cup N_{85} \cup N_{86} \cup N_{87} \cup N_{88} \cup N_{89} \cup N_{90} \cup N_{91} \cup N_{92} \cup N_{93} \cup N_{94} \cup N_{95} \cup N_{96} \cup N_{97} \cup N_{98} \cup N_{99} \cup N_{100}$$

11. 01 NOV 1994.
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 12. 01 MAY 1994: 94BP-4415998.
 XX
 13. 01 MAY 1994: 94BP-4415999.
 XX
 14. 01 MAY 1994: BAEF A1.
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 97. 01 MAY 1994: BAEF A1.
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 98. 01 MAY 1994: BAEF A1.
 XX
 99. 01 MAY 1994: BAEF A1.
 XX
 100. 01 MAY 1994: BAEF A1.
 XX

and treatment of blood disorders
 Example 1: Page 25: 10pp: English.
 The present sequence represents a peptide fragment of human erythropoietin (EPO), the present invention describes a method of producing human EPO which causes bone marrow cells to increase production of red blood cells or red blood cells, where the polypeptide is the product of expression in CHO (Chinese hamster ovary) cells of an expression DNA sequence encoding human EPO. EPO is present in the plasma in the diagnosis and treatment of blood disorders characterized by low or defective red blood cell production.
 Sequence 4 AA:
 Query Match: 65.00% Score: 1.00 (16.16) Length: 41
 Best local Similarity: 100.00% (16.16) (16.16)
 Matches: 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0
 1 VLE 4
 1 1 1 1
 1 VLE 4
 Search completed: October 28, 2002, 06:25:36
 Job time: 0:12:00

1 GENERAL INFORMATION
2 APPLICANT: Welter, Patrick
3 APPLICANT: Welter, Scott
4 APPLICANT: Kowak, John F.W.
5 APPLICANT: Kowak, John F.W.
6 APPLICANT: Zhang, Han Zhou
7 TITLE OF INVENTION: A Method of Producing a Protein Molecule and
8 TITLE OF INVENTION: Their Applications for Wheat Seed Treatments
9 TITLE OF INVENTION: Screening Assays for Gasparins and Their Enzymes and the
10 TITLE OF INVENTION: Use thereof
11 FILE REFERENCE: 1745,026,000Z
12 CURRENT APPLICATION NUMBER: 09/441,071
13 FILING DATE: 1998-10-09
14 EARLIER APPLICATION NUMBER: US 09/441,072
15 EARLIER FILING DATE: 1997-10-10
16 EARLIER APPLICATION NUMBER: US 09/441,073
17 EARLIER FILING DATE: 1998-04-04
18 NUMBER OF SEQ ID NOS: 142
19 SOFTWARE: Patent In Vitro 2.0
20 SEQ ID NO 25
21 TYPE: PRT
22 LENGTH: 4
23 ORGANISM: Artificial Sequence
24 FEATURE:
25 OTHER INFORMATION: Description of Artificial Sequence submitted for
26 OTHER INFORMATION: Poplids
27 US 09-732-411-15

Query Match: 70.0%; Score: 14; Pos: 4; Length: 4;
Best Local Similarity: 66.7%; Prod. No: 1,700,062;
Matches: 23; Conserved: 0; Mismatches: 0; Indels: 0; Type: 0;

27 2 SEP 4
28 1 SEP 4

103001 12
US 09-441-071-09
1 Sequence 20, Application US/09441071
2 Patent No. 645676
3 INVENTOR: Matthew David L.
4 APPLICANT: Welter, John A.
5 APPLICANT: Welter, Mark L.
6 TITLE OF INVENTION: Identification of No. 564676 and Substances
7 NUMBER OF SEQUENCES: 152
8 CORRESPONDENCE ADDRESS:
9 STREET: 400 Point San Bruno Blvd
10 CITY: South San Francisco
11 STATE: California
12 COUNTRY: USA
13 ZIP: 94080
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: 5.25 inch, 400 Kb floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: DOS/MS DOS
18 SOFTWARE: Patent (Computer)
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: 09/441,071
21 FILING DATE: 10 MAY 1998
22 CLASSIFICATION: 435
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: 09/441,072
25 FILING DATE: 09 APR 1998
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: 09/441,072
28 FILING DATE: 09 APR 1998

1 APPLICATION NUMBER: 09/441,071
2 FILING DATE: 09 DEC 1997
3 PRIOR APPLICATION DATA:
4 APPLICATION NUMBER: 09/441,072
5 FILING DATE: 09 AUG 1997
6 PRIOR APPLICATION DATA:
7 APPLICATION NUMBER: 09/441,073
8 FILING DATE: 14 JUN 1997
9 PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: 09/441,074
11 FILING DATE: 14 APR 1997
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER: 09/441,075
14 FILING DATE: 17 JUL 1997
15 PRIOR APPLICATION DATA:
16 APPLICATION NUMBER: 09/441,076
17 FILING DATE: 17 JUL 1997
18 APPLICATION NUMBER: 09/441,077
19 FILING DATE: 09 DEC 1997
20 APPLICATION NUMBER: 09/441,078
21 NAME: Welter, David L.
22 RESIDENCE NUMBER: 435,657
23 REFERENCE: 1745,026,000Z
24 TELEPHONE: 415/275-1249
25 TELEFAX: 415/275-1249
26 TELEFAX: 415/275-1249
27 TELEFAX: 415/275-1249
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Query Match: 66.0%; Score: 13; Pos: 2; Length: 4;
Best Local Similarity: 66.7%; Prod. No: 1,700,062;
Matches: 23; Conserved: 0; Mismatches: 0; Indels: 0; Type: 0;

27 2 SEP 4
28 1 SEP 4

103001 12
US 09-441-071-16
1 Sequence 17, Application US/09441071
2 Patent No. 645676
3 INVENTOR: Matthew David L.
4 APPLICANT: Welter, John A.
5 APPLICANT: Welter, Mark L.
6 TITLE OF INVENTION: Identification of No. 564676 and Substances
7 NUMBER OF SEQUENCES: 152
8 CORRESPONDENCE ADDRESS:
9 STREET: 400 Point San Bruno Blvd
10 CITY: South San Francisco
11 STATE: California
12 COUNTRY: USA
13 ZIP: 94080
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: 5.25 inch, 400 Kb floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: DOS/MS DOS
18 SOFTWARE: Patent (Computer)
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: 09/441,071
21 FILING DATE: 10 MAY 1998
22 CLASSIFICATION: 435
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: 09/441,072
25 FILING DATE: 09 APR 1998
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: 09/441,073
28 FILING DATE: 14 JUN 1997
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER: 09/441,074
31 FILING DATE: 14 APR 1997
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34 FILING DATE: 17 JUL 1997
35 PRIOR APPLICATION DATA:
36 APPLICATION NUMBER: 09/441,076
37 FILING DATE: 17 JUL 1997
38 APPLICATION NUMBER: 09/441,077
39 FILING DATE: 09 DEC 1997
40 APPLICATION NUMBER: 09/441,078
41 NAME: Welter, David L.
42 RESIDENCE NUMBER: 435,657
43 REFERENCE: 1745,026,000Z
44 TELEPHONE: 415/275-1249
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27 1 SEP 4
28 2 SEP 4

103001 14
US 09-441-071-04
1 Sequence 34, Application US/09441071

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1 147557 N 6146876
2 GENERAL INFORMATION:
3 APPLICANT: Kaplan, Keith E.
4 APPLICANT: Kapeller-Libermann, Rosana
5 APPLICANT: White, David
6 TITLE OF INVENTION: A No. 6146876el Human Cyclic Nucleosides
7 TITLE OF INVENTION: Phosphodiesterase
8 FILE REFERENCE: 5800 28
9 CURRENT APPLICANT: RIMMER, 02/09/99, 970
10 CURRENT FILING DATE: 1999-06-11
11 EARLIER APPLICATION NUMBER: 09/227,423
12 EARLIER FILING DATE: 1999-04-26
13 NUMBER OF SEQ ID NOS: 40
14 SOFTWARE: FastSeq for Windows Version 3.0
15 SEQ ID NO: 34
16 LENGTH: 4
17 TYPE: PRT
18 ORGANISM: Homo Sapiens
19 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24

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2007 Match 65.0% Score 13 DB 4 Length 4
Best Local Similarity 100.0% Pred. No. 1,700,000
Matches 4 Conserved 100 0 Mismatches 0 Gaps 0

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23 1 VIE 3
24 1 VIE 4

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1 147557 N 6146876
2 GENERAL INFORMATION:
3 APPLICANT: Albert C. Gyorkos
4 APPLICANT: Tyle W. Spruce
5 APPLICANT: Axel H. Leimer
6 APPLICANT: John C. Cheronis
7 TITLE OF INVENTION: Serine Protease Inhibitors Comprised
8 TITLE OF INVENTION: Alpha-Keto Heterocycles
9 FILE REFERENCE: 61249-006 (21 CIP)
10 CURRENT APPLICANT: RIMMER, 02/09/99, 970
11 CURRENT FILING DATE: 1997-05-20
12 EARLIER APPLICATION NUMBER: US 09/345,820
13 EARLIER FILING DATE: 1996-11-21
14 NUMBER OF SEQ ID NOS: 58
15 SOFTWARE: FastSeq for Windows Version 4.0
16 SEQ ID NO: 41
17 LENGTH: 4
18 TYPE: PRT
19 ORGANISM: Serine Protease
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2007 Match 65.0% Score 13 DB 4 Length 4
Best Local Similarity 100.0% Pred. No. 1,700,000
Matches 4 Conserved 100 0 Mismatches 0 Gaps 0

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23 1 VIE 3
24 1 VIE 4

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Search Completed: October 28, 2002, 06:27:53
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24

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Copyright (c) 1993-2002 Compuserp Inc.

10M protein - protein search, using SW model

Run on: October 28, 2002, 06:11:54 ; Search time: 15.36 sec.
(without formatting)
25,624 Million cell updates/sec

Filter: DS 09 732 411 15

Portion scored: 20

Sequences: 1 VLEP 4

Result filter: BL-SW02

Cutoff: 100.0 / expect 0.5

Searched: 20416 seqs, 9609344 residues

Number of hits satisfying chosen parameters: 20416

Minimum hit seq length: 1

Maximum hit seq length: 20000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listed first 45 summaries

Database:

1: prot1*

2: prot2*

3: prot3*

4: prot4*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result listed below, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query Match	Length	DB	ID	Accession
1	26	100.0	28	2	A27261	protease inhibitor 3, sea anemone (<i>Stelechodactyla</i> sp.) (Clamments)
2	26	100.0	47	2	S26227	protein P10 - curled leaved tobacco (Clamment)
3	26	100.0	58	2	S03610	protein P10 - curled leaved tobacco (Clamment)
4	26	100.0	59	2	R00242	protein P10 - curled leaved tobacco (Clamment)
5	26	100.0	59	2	A05296	protein P10 - curled leaved tobacco (Clamment)
6	26	100.0	61	2	I04065	protein P10 - curled leaved tobacco (Clamment)
7	26	100.0	62	2	S03621	protein P10 - curled leaved tobacco (Clamment)
8	26	100.0	63	2	R00962	protein P10 - curled leaved tobacco (Clamment)
9	26	100.0	68	2	S04444	protein P10 - curled leaved tobacco (Clamment)
10	26	100.0	77	2	S72645	protein P10 - curled leaved tobacco (Clamment)
11	26	100.0	80	2	I15296	protein P10 - curled leaved tobacco (Clamment)
12	26	100.0	85	2	R05324	protein P10 - curled leaved tobacco (Clamment)
13	26	100.0	82	2	I42093	protein P10 - curled leaved tobacco (Clamment)
14	26	100.0	83	2	I19712	protein P10 - curled leaved tobacco (Clamment)
15	26	100.0	86	2	R09197	protein P10 - curled leaved tobacco (Clamment)
16	26	100.0	89	2	R72296	protein P10 - curled leaved tobacco (Clamment)
17	26	100.0	92	2	JN0449	protein P10 - curled leaved tobacco (Clamment)
18	26	100.0	93	2	R06795	protein P10 - curled leaved tobacco (Clamment)
19	26	100.0	93	2	S40656	protein P10 - curled leaved tobacco (Clamment)
20	26	100.0	93	2	AE0923	protein P10 - curled leaved tobacco (Clamment)
21	26	100.0	93	2	I01217	protein P10 - curled leaved tobacco (Clamment)
22	26	100.0	93	2	R06063	protein P10 - curled leaved tobacco (Clamment)
23	26	100.0	99	2	I07093	protein P10 - curled leaved tobacco (Clamment)
24	26	100.0	101	2	I25656	protein P10 - curled leaved tobacco (Clamment)
25	26	100.0	102	2	S52711	protein P10 - curled leaved tobacco (Clamment)
26	26	100.0	103	2	R06554	protein P10 - curled leaved tobacco (Clamment)
27	26	100.0	103	2	R70060	protein P10 - curled leaved tobacco (Clamment)
28	26	100.0	106	1	Q0MKEP	protein P10 - curled leaved tobacco (Clamment)
29	26	100.0	106	2	S04150	protein P10 - curled leaved tobacco (Clamment)

30	26	100.0	105	2	AE1449	hypothetical protein
31	26	100.0	105	2	S76770	hypothetical protein
32	26	100.0	106	2	R01609	conserved hypothetical protein
33	26	100.0	108	2	I13153	protein sp46, Pba
34	26	100.0	108	2	I41447	very hypothetical protein
35	26	100.0	109	2	R06657	hypothetical protein
36	26	100.0	111	2	I72112	hypothetical protein
37	26	100.0	111	2	R05111	hypothetical protein
38	26	100.0	112	2	R09408	hypothetical protein
39	26	100.0	112	2	I00406	hypothetical protein
40	26	100.0	113	2	R00319	hypothetical protein
41	26	100.0	114	2	R07413	nitrogen regulation
42	26	100.0	115	2	I72710	hypothetical protein
43	26	100.0	115	2	R04326	hypothetical protein
44	26	100.0	116	1	Q04SH0	hypothetical protein
45	26	100.0	116	1	Q04SH0	hypothetical protein

ALIGNMENTS

PEP11 1

A27261

Protease inhibitor 3, sea anemone (*Stelechodactyla* sp.) (Clamments)

Species: *Stelechodactyla* sp.; Stachetis sp.

Created: 31 Mar 1989 #sequence_revision 41 Mar 1989 #text_change 19 Jan 1999

Accession: A27261

Notes: D. Gehan, E.

Toxin 20, 845, 1992

Alti: Structural studies on a protease inhibitor from the sea anemone *Stelechodactyla*

Accession number: A27261

Accession: A27261

Molecule type: protein

Accession: 1 28 -ME3

Query Match:

Best Local Similarity: 100.00%; Score: 26; Length: 28;

Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 VLEP 4

DB 4 VLEP 7

RESULT 2

Q26027

protein P10 - curled leaved tobacco (Clamment)

Species: *Nicotiana glauca* (curled leaved tobacco)

Created: 19 May 1989 #sequence_revision 19 May 1989 #text_change 11 Jan 2000

Accession: Q26027

Notes: D. Gehan, E. Van der Kerkhof, J.

Protein, N. L. Acad. Sci. U.S.A. 94, 4806-4810, 1997

Alti: Alterations in the phenotype of plant cells stably NH₂ terminal, anho

Accession number: Q26027

Molecule type: protein

Accession: 1-47 -R001

Superfamily: Thaumatin 1

Query Match:

Best Local Similarity: 100.00%; Score: 27; Length: 47;

Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 VLEP 4

DB 29 VLEP 42

RESULT 3

S00010

protein P10 - curled leaved tobacco (Clamment)

Species: *Nicotiana glauca* (curled leaved tobacco)

Created: 28 Feb 1990 #sequence_revision 28 Feb 1990 #text_change 11 Jan 2000

A: Accession No. 141904
F: Field collection locality: Forested hill, lowland forest;
A: Age: 7-8 years; sex: ♀
A: Host: 1-62 N12.
A: Tissue references: EMBL4430; FJIN-AA04764.1
A: External source: Strain J1
A: Ref test: GN1
A: Accession No. 142004
A: Status: preliminary; Forested hill, CR/EMU/GN1
A: Accession type: UNA
A: Accession: 1-62 N1C.
A: Tissue references: EMB44440; FJIN-AA04764.1
A: External source: Strain J1
A: Ref test: GN2
A: Ref test: GN1
A: Ref: Hx
A: Map position: 3976-4224
A: Coordinates: 8GN2
A: Ref: Hx
Map position: 143028-143271


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Best local Similarity: 100.0%; Prod. No. 14942;
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 VLEP 4
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IR 4 VLEP 94

RESULT 6
RP Z_L18A;
RP PROTEIN; STAMPA; PPT. 98 AA.
AA 44VVI;
QY 16-01-2001 (Rel. 40, Created)
IR 16-01-2001 (Rel. 41, Last annotation update)
DE RNA directed RNA polymerase alpha chain (RP 2056669) (transcriptase
LE alpha chain) (RNA polymerase alpha subunit)
GN RP07
CC Bacteria; Thermus; alpha; reverse transcriptase. The alpha subunit of the
CC NBL_LaxID=271;
CC (1)
RN SEQUENCE FROM N.A.
RX MEDLINE=2056669; PubMed 11114402;
RA Manaklin L., Bhagat S., Brunning A., Campbell E.A., Parst S.A.,
RA Bright P.H., Severinov K.
RA "Bacterial RNA polymerase subunit alpha and subunit epsilon polymerase
RI subunit RP66 are sequence, structural, and functional homologs and
RI promote RNA polymerase assembly."
RI Proc. Natl. Acad. Sci. U.S.A. 98:992-997(2001).
CC (-) FUNCTION: Promotes RNA polymerase assembly. Interacts the N- and C-
CC terminal regions of the beta' subunit thereby facilitating the N-
CC interaction with the beta and alpha subunits.
CC (-) CATALYTIC ACTIVITY: N nucleoside triphosphate + N-4-thiophosphate
CC [RNA](N).
CC (-) SUBUNIT: COMPLEX OF A ALPHA SUBUNIT AND THE RNA POLYMERASE BETA
CC AND COMPLEXES OF 2 ALPHA CHAINS. 1 BETA CHAIN. 1 ALPHA CHAIN AND 1
CC OMEGA CHAIN.
CC (-) SIMILARITY: RELATED TO THE RNA POLYMERASE BETA CHAIN REGION.
CC THIS SWISS-PROT entry is a copy of the N-terminus of the alpha subunit of
CC between the Swiss Institute of Bioinformatics and the EMBL annotation
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed, usurped by, and for commercial
CC purposes replaced in any way. For more information see the EMBL
CC or send an email to license@lsb.scrib.ch).
IR RM001_A195436; CO-1549 137;
RW TRANSCRIPTASE; RNA directed RNA polymerase; Transcription
PI INLIMET 0
SL SEQUENCE 98 AA; 11494 MW; 8E429F148B6266; CDS:41;

Best local Similarity: 100.0%; Score 20; Indel: 0; Gaps: 0;
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 VLEP 4
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IR 48 VLEP 41

RESULT 7
VLEP41;
IR V39_40B3
AA 54789;

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IR 15 DEC 1998 (Rel. 37, Created)
IR 15 DEC 1998 (Rel. 37, Last annotation update)
IR 15 DEC 1998 (Rel. 37, Last annotation update)
DE Early protein GP6;
GN GP6
CC Bacteriophage B104;
CC VIRUSES; dsDNA viruses, no RNA stage; Caudovirales; Podovirinae.
CC NBL_LaxID=10776;
CC (1)
RN SEQUENCE FROM N.A.
RX MEDLINE=9901981; PubMed 949827;
RA Pavlovskaya T., Jones V., Paves J., Vleck C., Paves V.
RA "Bacteriophage B104: complete DNA sequence of its genome and
RI relationship to other Bacillus phages."
RI Gene 193:157-163(1997).
CC (-) FUNCTION: RESISTANCE TO VIRAL DNA REPLICATION. ACTIVATES THE
CC INITIATION OF DNA REPLICATION BY FORMING A HELICASE
CC NUCLEOPROTEIN COMPLEX AT THE REPLICATIVE ORIGIN (BY SIMILARITY).
CC THIS SWISS-PROT entry is a copy of the N-terminus of the alpha subunit of
CC between the Swiss Institute of Bioinformatics and the EMBL annotation
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed, usurped by, and for commercial
CC purposes replaced in any way. For more information see the EMBL
CC or send an email to license@lsb.scrib.ch).
IR RM01_X99250; CAA67653.1;
RW Early protein; DNA replication.
SL SEQUENCE 130 AA; 11357 MW; 3FA24866445808; CDS:4;

Query Match: 100.0%; Score 20; Indel: 0; Gaps: 0;
Best local Similarity: 100.0%; Prod. No. 14942;
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 VLEP 4
   |||
IR 40 VLEP 43

RESULT 8
V592_OHLN
IR V592_OHLN; CAA6565;
AA Q97W27; Q9K202;
DI 16-01-2001 (Rel. 40, Created)
IR 16-01-2001 (Rel. 41, Last annotation update)
DI 01 MAR 2002 (Rel. 41, Last annotation update)
IR 01 MAR 2002 (Rel. 41, Last annotation update)
DE Bacterial protein; Bacteriophage; Bacteriophage;
GN V592_OHLN; CAA6565; OR Q9K202;
CC Bacteria; Chlamydiales; Chlamydiales; Chlamydiales.
CC NBL_LaxID=84558;
CC (1)
RN SEQUENCE FROM N.A.
RX SRAIN_OHL029;
RX MEDLINE=925553; PubMed 119209;
RA Kato M., Mitchell W., Marathe K., Lammert C., Pan J., Hyman F.W.,
RA Oliner L., Grimwood J., Davis R.W., Stephens R.S.
RA "Comparative genomes of Chlamydia pneumoniae and Chlamydia
RI Nat. Genet. 21:486-489(1999).
CC (2)
RN SEQUENCE FROM N.A.
RX SRAIN_OHL029;
RX MEDLINE=20150255; PubMed 10694086;
RA Read T.D., Brumham R.C., Shen C., Gill S.R., Reidelberg J.P.,
RA White C., Hickey R.K., Peterson J., O'Brien K.L., Berry K., Bass S.,
RA Linder K., Weisman J., Khouri H., O'Brien B., Bergman C., Baskin E.,
RA Giam M., Nelson W., Kelly K., Kozlov A., Melnyk G., Scharf S.,
RA Elsen J., Fraser C.M.
RA "Genome sequences of Chlamydia trachomatis Mefn and Chlamydia
RI pneumoniae AR39."
RI Nucleic Acids Res. 28:1497-1496(2000).
IR [4]

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2009 Math 400.08, Sec 20, 16.1, 16.2, 16.3, 16.4, 16.5, 16.6, 16.7, 16.8, 16.9, 16.10, 16.11, 16.12, 16.13, 16.14, 16.15, 16.16, 16.17, 16.18, 16.19, 16.20, 16.21, 16.22, 16.23, 16.24, 16.25, 16.26, 16.27, 16.28, 16.29, 16.30, 16.31, 16.32, 16.33, 16.34, 16.35, 16.36, 16.37, 16.38, 16.39, 16.40, 16.41, 16.42, 16.43, 16.44, 16.45, 16.46, 16.47, 16.48, 16.49, 16.50, 16.51, 16.52, 16.53, 16.54, 16.55, 16.56, 16.57, 16.58, 16.59, 16.60, 16.61, 16.62, 16.63, 16.64, 16.65, 16.66, 16.67, 16.68, 16.69, 16.70, 16.71, 16.72, 16.73, 16.74, 16.75, 16.76, 16.77, 16.78, 16.79, 16.80, 16.81, 16.82, 16.83, 16.84, 16.85, 16.86, 16.87, 16.88, 16.89, 16.90, 16.91, 16.92, 16.93, 16.94, 16.95, 16.96, 16.97, 16.98, 16.99, 17.00, 17.01, 17.02, 17.03, 17.04, 17.05, 17.06, 17.07, 17.08, 17.09, 17.10, 17.11, 17.12, 17.13, 17.14, 17.15, 17.16, 17.17, 17.18, 17.19, 17.20, 17.21, 17.22, 17.23, 17.24, 17.25, 17.26, 17.27, 17.28, 17.29, 17.30, 17.31, 17.32, 17.33, 17.34, 17.35, 17.36, 17.37, 17.38, 17.39, 17.40, 17.41, 17.42, 17.43, 17.44, 17.45, 17.46, 17.47, 17.48, 17.49, 17.50, 17.51, 17.52, 17.53, 17.54, 17.55, 17.56, 17.57, 17.58, 17.59, 17.60, 17.61, 17.62, 17.63, 17.64, 17.65, 17.66, 17.67, 17.68, 17.69, 17.70, 17.71, 17.72, 17.73, 17.74, 17.75, 17.76, 17.77, 17.78, 17.79, 17.80, 17.81, 17.82, 17.83, 17.84, 17.85, 17.86, 17.87, 17.88, 17.89, 17.90, 17.91, 17.92, 17.93, 17.94, 17.95, 17.96, 17.97, 17.98, 17.99, 18.00, 18.01, 18.02, 18.03, 18.04, 18.05, 18.06, 18.07, 18.08, 18.09, 18.10, 18.11, 18.12, 18.13, 18.14, 18.15, 18.16, 18.17, 18.18, 18.19, 18.20, 18.21, 18.22, 18.23, 18.24, 18.25, 18.26, 18.27, 18.28, 18.29, 18.30, 18.31, 18.32, 18.33, 18.34, 18.35, 18.36, 18.37, 18.38, 18.39, 18.40, 18.41, 18.42, 18.43, 18.44, 18.45, 18.46, 18.47, 18.48, 18.49, 18.50, 18.51, 18.52, 18.53, 18.54, 18.55, 18.56, 18.57, 18.58, 18.59, 18.60, 18.61, 18.62, 18.63, 18.64, 18.65, 18.66, 18.67, 18.68, 18.69, 18.70, 18.71, 18.72, 18.73, 18.74, 18.75, 18.76, 18.77, 18.78, 18.79, 18.80, 18.81, 18.82, 18.83, 18.84, 18.85, 18.86, 18.87, 18.88, 18.89, 18.90, 18.91, 18.92, 18.93, 18.94, 18.95, 18.96, 18.97, 18.98, 18.99, 19.00, 19.01, 19.02, 19.03, 19.04, 19.05, 19.06, 19.07, 19.08, 19.09, 19.10, 19.11, 19.12, 19.13, 19.14, 19.15, 19.16, 19.17, 19.18, 19.19, 19.20, 19.21, 19.22, 19.23, 19.24, 19.25, 19.26, 19.27, 19.28, 19.29, 19.30, 19.31, 19.32, 19.33, 19.34, 19.35, 19.36, 19.37, 19.38, 19.39, 19.40, 19.41, 19.42, 19.43, 19.44, 19.45, 19.46, 19.47, 19.48, 19.49, 19.50, 19.51, 19.52, 19.53, 19.54, 19.55, 19.56, 19.57, 19.58, 19.59, 19.60, 19.61, 19.62, 19.63, 19.64, 19.65, 19.66, 19.67, 19.68, 19.69, 19.70, 19.71, 19.72, 19.73, 19.74, 19.75, 19.76, 19.77, 19.78, 19.79, 19.80, 19.81, 19.82, 19.83, 19.84, 19.85, 19.86, 19.87, 19.88, 19.89, 19.90, 19.91, 19.92, 19.93, 19.94, 19.95, 19.96, 19.97, 19.98, 19.99, 20.00, 20.01, 20.02, 20.03, 20.04, 20.05, 20.06, 20.07, 20.08, 20.09, 20.10, 20.11, 20.12, 20.13, 20.14, 20.15, 20.16, 20.17, 20.18, 20.19, 20.20, 20.21, 20.22, 20.23, 20.24, 20.25, 20.26, 20.27, 20.28, 20.29, 20.30, 20.31, 20.32, 20.33, 20.34, 20.35, 20.36, 20.37, 20.38, 20.39, 20.40, 20.41, 20.42, 20.43, 20.44, 20.45, 20.46, 20.47, 20.48, 20.49, 20.50, 20.51, 20.52, 20.53, 20.54, 20.55, 20.56, 20.57, 20.58, 20.59, 20.60, 20.61, 20.62, 20.63, 20.64, 20.65, 20.66, 20.67, 20.68, 20.69, 20.70, 20.71, 20.72, 20.73, 20.74, 20.75, 20.76, 20.77, 20.78, 20.79, 20.80, 20.81, 20.82, 20.83, 20.84, 20.85, 20.86, 20.87, 20.88, 20.89, 20.90, 20.91, 20.92, 20.93, 20.94, 20.95, 20.96, 20.97, 20.98, 20.99, 21.00, 21.01, 21.02, 21.03, 21.04, 21.05, 21.06, 21.07, 21.08, 21.09, 21.10, 21.11, 21.12, 21.13, 21.14, 21.15, 21.16, 21.17, 21.18, 21.19, 21.20, 21.21, 21.22, 21.23, 21.24, 21.25, 21.26, 21.27, 21.28, 21.29, 21.30, 21.31, 21.32, 21.33, 21.34, 21.35, 21.36, 21.37, 21.38, 21.39, 21.40, 21.41, 21.42, 21.43, 21.44, 21.45, 21.46, 21.47, 21.48, 21.49, 21.50, 21.51, 21.52, 21.53, 21.54, 21.55, 21.56, 21.57, 21.58, 21.59, 21.60, 21.61, 21.62, 21.63, 21.64, 21.65, 21.66, 21.67, 21.68, 21.69, 21.70, 21.71, 21.72, 21.73, 21.74, 21.75, 21.76, 21.77, 21.78, 21.79, 21.80, 21.81, 21.82, 21.83,

- 2 - ; V.I.P. 4 ; V.I.P. 7 ;

[illegible]

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AF01510	ARF1510		
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AF01605	ARF1605		

Archaeoglobus fulgidus,
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A-600,
Archaeoglobus fulgidus,
NCTC 10740, 2387.

[illegible][illegible]

— 100 —

SNOW, P. W., P. ANDERSON, R. P. FRIEDMAN, C. J. FELLER, S. G. MATHIAS, AND R. P. REED. 1990. *Archaeobacillus* sp. n., a thermophilic, anaerobic, acid-producing bacterium from a hydrothermal vent. *Journal of Geophysical Research* 95:12,339-12,346.

SNOW, P. W., P. ANDERSON, R. P. FRIEDMAN, C. J. FELLER, S. G. MATHIAS, AND R. P. REED. 1991. The complete genome sequence of the hyperthermophilic archaeobacter, *Archaeobacillus* sp. n. *Science* 254:464-470 (1991).

[illegible]

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57

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 FROM: AES00098; AAR89743.1
 TO: AF1587;
 RE: Reparatase 194 protein; Complete proteins.

[illegible]

Σ

Category	Number of Responses	Percentage of Responses
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2. VLEP 85	1111	100.00

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	3
2	2
-	1
	0
2	9
-	8
	7
2	6
-	5
	4
2	3
-	2
	1
2	0
-	9
	8
2	7
-	6
	5
2	4
-	3
	2
2	1
-	0
	9
2	8
-	7
	6
2	5
-	4
	3
2	2
-	1
	0
2	9
-	8
	7
2	6
-	5
	4
2	3
-	2
	1
2	0
-	9
	8
2	7
-	6
	5
2	4
-	3
	2
2	1
-	0
	9
2	8
-	7
	6
2	5
-	4
	3
2	2
-	1
	0
2	9
-	8
	7
2	6
-	5
	4
2	3
-	2
	1
2	0
-	9
	8
2	7
-	6
	5
2	4
-	3
	2
2	1
-	0
	9
2	8
-	7
	6
2	5
-	4
	3
2	2
-	1
	0
2	9
-	8
	7
2	6
-	5
	4
2	3
-	2
	1
2	0
-	9
	8
2	7
-	6
	5
2	4
-	3
	2
2	1</

2000

[illegible]

Matches: 4; Conservative: 0; Mismatches: 0; Indels: 1; Gaps: 0;

VF: 1 VLEN: 4

FF: 46 VLEN: 49

Search completed: October 28, 2002, 06:17:21
JUL: 1360: 29 secs

Genome version 5.1.4
Copyright (c) 1994-2002 Compugen Ltd.

EM protein: protein search, using SW model

Parameters: October 26, 2002, 04:11:25 : Search time: 0.3 seconds
(with built-in database)
9,105,811,366, 500,000,000, 2000

Filter: US 00 142 411 15

Best hit score: 20

Sequence: 1 VLEP 4

Search hit table: RESUME 2
1494 1 20 4 100 100 100

Searches: 0.2222 seqs, 172,949,229 residues

Total number of hits calculated: 172,949,229

Maximum hit seq length: 1

Maximum hit seq length: 200000000

Post processing: Minimum Match ok

Maximum Match look

Listed First 45 summaries

Database: 1 SP-archaeo

1: SP-archaeo

2: SP-archaeo

3: SP-archaeo

4: SP-archaeo

5: SP-archaeo

6: SP-archaeo

7: SP-archaeo

8: SP-archaeo

9: SP-archaeo

10: SP-archaeo

11: SP-archaeo

12: SP-archaeo

13: SP-archaeo

14: SP-archaeo

15: SP-archaeo

16: SP-archaeo

17: SP-archaeo

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	25	Q08M55	Q08M55, chlamydia
2	20	100.0	26	Q08M52	Q08M52, chlamydia
3	20	100.0	30	Q08M19	Q08M19, chlamydia
4	20	100.0	44	Q08M16	Q08M16, chlamydia
5	20	100.0	47	Q08M07	Q08M07, chlamydia
6	20	100.0	47	Q08M06	Q08M06, chlamydia
7	20	100.0	47	Q08M05	Q08M05, chlamydia
8	20	100.0	52	Q08M04	Q08M04, chlamydia
9	20	100.0	53	Q08M03	Q08M03, chlamydia
10	20	100.0	58	Q08M02	Q08M02, chlamydia
11	20	100.0	58	Q08M01	Q08M01, chlamydia
12	20	100.0	61	Q08M00	Q08M00, chlamydia
13	20	100.0	64	Q08M99	Q08M99, chlamydia
14	20	100.0	64	Q08M98	Q08M98, chlamydia
15	20	100.0	64	Q08M97	Q08M97, chlamydia
16	20	100.0	64	Q08M96	Q08M96, chlamydia

Prod. No. is the number of results predicted by chlamydia, based on a score greater than or equal to the score of the lowest ranked hit, and is derived by multiplying the total number of hits by 100.

Result 1	ID	Q08M55	PRELIMINARY	PR1	25 AA
Q08M55	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
10	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
11	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
12	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
13	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
14	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
15	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
16	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
17	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
18	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
19	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
20	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
21	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
22	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
23	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
24	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
25	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
26	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
27	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
28	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
29	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
30	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
31	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
32	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
33	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
34	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
35	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
36	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
37	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
38	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
39	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
40	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
41	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
42	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
43	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
44	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
45	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55

ALIGNMENTS

Query Match	Best local similarity	100.0%	Score 20	100.0%	Length 25
Matches	4	conservation	0	mismatches	0
QY	1 VLEP 4				
DB	2 V: 4				
RESULT 2					
Q08M55	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
10	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
11	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
12	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
13	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
14	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
15	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
16	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
17	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
18	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
19	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
20	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
21	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
22	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
23	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
24	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
25	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
26	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
27	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
28	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
29	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
30	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
31	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
32	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
33	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
34	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
35	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
36	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
37	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
38	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
39	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
40	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
41	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
42	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
43	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
44	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
45	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55

Query Match	Best local similarity	100.0%	Score 20	100.0%	Length 25
Matches	4	conservation	0	mismatches	0
QY	1 VLEP 4				
DB	2 V: 4				
RESULT 2					
Q08M55	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
10	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
11	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
12	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
13	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
14	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
15	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
16	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
17	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
18	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
19	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
20	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
21	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
22	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
23	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
24	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
25	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
26	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
27	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
28	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
29	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
30	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
31	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
32	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
33	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
34	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
35	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
36	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
37	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
38	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
39	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
40	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
41	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
42	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
43	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
44	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55
45	Q08M55	Q08M55	Q08M55	Q08M55	Q08M55

